

# SEQUENCE LISTING

(1) GENERAL INFORMATION:  
(iii) NUMBER OF SEQUENCES: 5

(2) INFORMATION FOR SEQ ID No: 1  
(i) CHARACTERISTICS OF THE SEQUENCE:

(A) LENGTH:

(B) TYPE: nucleotide

(C) NUMBER OF STRANDS: double

(D) CONFIGURATION: linear

(ii) TYPE OF MOLECULE: DNA

(ix) CHARACTERISTICS

(A) NAME/KEY:

(xi) DESCRIPTION OF THE SEQUENCES: SEQ ID No: 1:

GAATTCAGAT GCCTCATACC TTGGGATTAA AAAATTGATG TTCATTTGTT ATATATCCTG	60
GGCGGACAGG CCGGCTCGTA TTCTTCAGGG GTGTGCGCTA CCCAGTGCAC AGGAGGTTCC	120
GGAGGTGTCT TGGATGGAAA GTAAGGCCAT TTGTGGGTTC TCATCCATGT CATCGTCCCT	180
TTCGGCTGTT TCACCAAGAT CCAATTATTC CTCCAGGACT TTCAACCCTC AGAATGGAAA	240
CAGAGATGAA ACTCTCTGTG CAAATCGTAG ATATCGATTG GAGACATTGA AACCACGGAG	300
TTTGAAATAA AAGTATAAAT ACCTCCGAAA ACGCAGAGTT TAAG ATG AAA GGT ATT	356
	Met Lys Gly Ile
	1
TCT AAG ATC CTC TCT GCC TCT ATT GCC CTG ATG AAG TTG GAG AAT GTC	404
Ser Lys Ile Leu Ser Ala Ser Ile Ala Leu Met Lys Leu Glu Asn Val	
5 10 15 20	
TAT TCA GCA ACC GCA CTG TGC AGC AAT GCA TAT GGC CTA ACT CCG GGA	452
Tyr Ser Ala Thr Ala Leu Cys Ser Asn Ala Tyr Gly Leu Thr Pro Gly	
25 30 35	
CAA CAG GGT ATG GCT CAG CAG CCG TCG TAT GTG CTG ATC CCC AGC ACC	500
Gln Gln Gly Met Ala Gln Gln Pro Ser Tyr Val Leu Ile Pro Ser Thr	
40 45 50	
CCG GGA ACC ATA GCA AAC TGT GCA AGC GGT TCA CAG GAC ACA TAT TCT	548
Pro Gly Thr Ile Ala Asn Cys Ala Ser Gly Ser Gln Asp Thr Tyr Ser	
55 60 65	
CCT TCT CCC GCT GCA CCC ACA TCT CCA GTG ACT CCG GGG AAA ACT AGC	596
Pro Ser Pro Ala Ala Pro Thr Ser Pro Val Thr Pro Gly Lys Thr Ser	
70 75 80	
GAG AAT GAG ACA TCT CCA TCG GCT CCT GCA GAA GAT GTA GGA ACA TGC	644
Glu Asn Glu Thr Ser Pro Ser Ala Pro Ala Glu Asp Val Gly Thr Cys	
85 90 95 100	
AAG ATT GCC GTA TTG AAG CAC TGC GAC GCA CCA GGA ACA ACA TCA GGG	692
Lys Ile Ala Val Leu Lys His Cys Asp Ala Pro Gly Thr Thr Ser Gly	
105 110 115	

ACG ACA CCA GGG TCA GGG CCT TGT GAA ACC CCA GAG CAG CAA CAG CCT	740
Thr Thr Pro Gly Ser Gly Pro Cys Glu Thr Pro Glu Gln Gln Gln Pro	
120 125 130	
TTG TCA GTG ATC TCC ACC ACT CCT GCC GTA CCG GTG ACT GTG GAG TCT	788
Leu Ser Val Ile Ser Thr Thr Pro Ala Val Pro Val Thr Val Glu Ser	
135 140 145	
GCA CAG TCT CCA TCT GTT GTG CCA GTT GTT CCT GTC GTT GCT CAC CAC	836
Ala Gln Ser Pro Ser Val Val Pro Val Val Pro Val Val Ala His His	
150 155 160	
CAG GCA GTT CCA GGC TAC TAC AAC AAT GGA ACA TCC GGT ATT CCT GGA	884
Gln Ala Val Pro Gly Tyr Tyr Asn Asn Gly Thr Ser Gly Ile Pro Gly	
165 170 175 180	
CAG CAA CAG ATC CTT TCT GGC ACT CTT CCC CCA GGA GCC ACT TTG TGT	932
Gln Gln Gln Ile Leu Ser Gly Thr Leu Pro Pro Gly Ala Thr Leu Cys	
185 190 195	
CAG GGA CAG GCC ATG CCT AGC ACT CCT GGA CAG CAA CAG ATC CTT TCT	980
Gln Gly Gln Ala Met Pro Ser Thr Pro Gly Gln Gln Gln Ile Leu Ser	
200 205 210	
GGC ACT CTT CCC CCA GGG GTC ACT TTG TGT CAG GGA CAG GCC ACG CCT	1028
Gly Thr Leu Pro Pro Gly Val Thr Leu Cys Gln Gly Gln Ala Thr Pro	
215 220 225	
AGC ACT CCT GGG CAG CAA CAG GTC CTT TCT GGC ACT CTT CCC CCA GGA	1076
Ser Thr Pro Gly Gln Gln Gln Val Leu Ser Gly Thr Leu Pro Pro Gly	
230 235 240	
GTC ACT TTG TGT CAG GGA CAG GCC ACG CCT AGC ACT CCT GGG CAG CAA	1124
Val Thr Leu Cys Gln Gly Gln Ala Thr Pro Ser Thr Pro Gly Gln Gln	
245 250 255 260	
CAG GTC CTT TCT GGC ACC CTT CTC CCA GGA GCC ACT TTG TGT CAG GAT	1172
Gln Val Leu Ser Gly Thr Leu Leu Pro Gly Ala Thr Leu Cys Gln Asp	
265 270 275	
CAA GGT ATG CCT GGA ACA TCC GGA GTT CCT GGA CAG CAG GGA CAG TCT	1220
Gln Gly Met Pro Gly Thr Ser Gly Val Pro Gly Gln Gln Gly Gln Ser	
280 285 290	
AGT GGA CAG TGT TGT GCC CCT CAG ATT CCA AAC CCT GTC ATG CCG CCA	1268
Ser Gly Gln Cys Cys Ala Pro Gln Ile Pro Asn Pro Val Met Pro Pro	
295 300 305	
TCC ATG AAC ATT AGT GGA AAT GGG TAT CCT TCT TCT ACC GCA TAC AGC	1316
Ser Met Asn Ile Ser Gly Asn Gly Tyr Pro Ser Ser Thr Ala Tyr Ser	
310 315 320	
CCA AAC CTC GGA TCA CTG GGA TCC TGT GTT GAC ATA CAG AAG ACG GGG	1364
Pro Asn Leu Gly Ser Leu Gly Ser Cys Val Asp Ile Gln Lys Thr Gly	
325 330 335 340	
GGG ACA TCC TGC GAG CAA AAA CCC GAG AAG TCC GCC ACG CAG TAT GCC	1412
Gly Thr Ser Cys Glu Gln Lys Pro Glu Lys Ser Ala Thr Gln Tyr Ala	
345 350 355	

ATG GAG GCC TGT GCA ACA CCA ACA CCA ACG GTT ATT ATA GGC AAC AGC	1460
Met Glu Ala Cys Ala Thr Pro Thr Pro Thr Val Ile Ile Gly Asn Ser	
360 365 370	
GAG TAT CTT GTT GGA CCA GGA ATG TAC AAT GCA ATT AAC TCT CCA TGC	1508
Glu Tyr Leu Val Gly Pro Gly Met Tyr Asn Ala Ile Asn Ser Pro Cys	
375 380 385	
AAC ACT GCT GTC CAA TGC TGC TAG GCTAAAATAA AACGAGTTTA ATCTTCTTTT	1562
Asn Thr Ala Val Gln Cys Cys	
390 395	
TCTTCGGTCT TTTGGAACGT TGGATGGGGA TGGAGGAGTC TATGGGCTGA AGTGAAATGC	1622
CAACACTTCT TCTGCCCAAG AACACATTCTG GATGTTCTTC CTGTGGCCAG GAGTTTGGA	1682
ACAGGATTCC CCGAGGATTT AGCAGCCTTG GAGTACCATG ATTGAATCAG TATTAAACTT	1742
CTCAAATTAT TTTATTCTTT CTGTTTTATA TCCCGAGCCA ATCTGAGAAG AATGCCTCGA	1802
ATTCAAGCTC CCTTAGAAGT GTGGGATC	1830

## (2) INFORMATION FOR SEQ ID No: 2

### (i) CHARACTERISTICS OF THE SEQUENCE:

#### (A) LENGTH:

#### (B) TYPE: nucleotide

#### (C) NUMBER OF STRANDS: double

#### (D) CONFIGURATION: linear

#### (ii) TYPE OF MOLECULE: DNA

#### (ix) CHARACTERISTICS

#### (A) NAME/KEY:

### (xi) DESCRIPTION OF THE SEQUENCES: SEQ ID No: 2:

AAGCTTCTGA ACAAGCGCTA ACCCTCTTTC AGAATATATA AAGCAATCCA TACAACCTCT	60
CCATCCATCC CGGTGCTGTT TCTTTGGAGG CAAAACAGAG GAGGTGGCGA TATCGATGGT	120
GCATCCATAA TATATACAAG ACACTCCAGG CTGCAACTGA ATCAACACAC TCCATCCCCCT	180
CAGGAAGTCG GTAAACTTGC CTTGAAAATA GCCAATGGAT GTCTCCAGGC TTTATACCAT	240
GCACAGCTAT ATCTTGGCCT GAAGTGCACCT TTCAGGTGGG GCTTTGTTAC ATTGCGGTGT	300
TTTGGATTAC CTGATATAAT TTGTTACCCA CTGAGTCAAG TCGAAACCAG TAGTCCGCAG	360
ATTTCTAACA GAGAGGAAAG ACTGGAGGTA ATTTGTGGCT TTTGAAACAT GCACAGCAAA	420
ATAAAATATA AAAGAAGCCT TTTGCACACT ACCAAAG ATG TTG TTA CTT CTC GCC	475
Met Leu Leu Leu Leu Ala	
1 5	
ATA ACT GCT GTT GTT AGC GCC ACG ATG GTC CAT CCT TCA GCT GTT GTT	523
Ile Thr Ala Val Val Ser Ala Thr Met Val His Pro Ser Ala Val Val	
10 15 20	
CCA CAG CCC GCA GCA CCT CTC CAT GTC GTT CCC CCA CAG CAG CAA ATG	571
Pro Gln Pro Ala Ala Pro Leu His Val Val Pro Pro Gln Gln Gln Met	
25 30 35	
GGC ATG GTT AAC GGA TGC ACC AGC AAG AAA CTA GAG GGT GCA GAA ATA	619
Gly Met Val Asn Gly Cys Thr Ser Lys Lys Leu Glu Gly Ala Glu Ile	
40 45 50	

ATG AGA AGG AAC ATG ATT GAG TGC CAG AAA AGA AGC TCG GAG GCA ACA	667
Met Arg Arg Asn Met Ile Glu Cys Gln Lys Arg Ser Ser Glu Ala Thr	
55 60 65 70	
AAG GCG ATG ATT GAA AGG GCA AAT GAA AAG GCT GTA GAA TCA TTC AAC	715
Lys Ala Met Ile Glu Arg Ala Asn Glu Lys Ala Val Glu Ser Phe Asn	
75 80 85	
AAG GAA GTT AGC AAA GGA CCT AGC CAA AAG GAT GGA GGC CAG TGC ATA	763
Lys Glu Val Ser Lys Gly Pro Ser Gln Lys Asp Gly Gly Gln Cys Ile	
90 95 100	
GAA AAA GCT GTA CAA GGT ACC GAT AGG TGT ATT CTC GCT GGA ATA ATC	811
Glu Lys Ala Val Gln Gly Thr Asp Arg Cys Ile Leu Ala Gly Ile Ile	
105 110 115	
GAT AAG GCG GTG AAC AAG CGC AAG TAC AGA ATC TCA GAT GTG GAG AAC	859
Asp Lys Ala Val Asn Lys Arg Lys Tyr Arg Ile Ser Asp Val Glu Asn	
120 125 130	
AGC ACC TCG CTC TAC AGA GGA GAC AAG CTA ATT GCC CTA ATT GTC AAT	907
Ser Thr Ser Leu Tyr Arg Gly Asp Lys Leu Ile Ala Leu Ile Val Asn	
135 140 145 150	
GTC GAC TAT GGG CTG CAG CCG ATC ACT AAG CCA AAG AAG AAG TCC	955
Val Asp Tyr Gly Leu Gln Pro Ile Thr Lys Pro Lys Lys Lys Ser	
155 160 165	
AAG ATA ATG GCG AAT CTC CCT CAG CCG AAG AGA GAG ATG TAT TTC AAC	1003
Lys Ile Met Ala Asn Leu Pro Gln Pro Lys Arg Glu Met Tyr Phe Asn	
170 175 180	
CAA ATC GGT CAG CTT GTT GGA GCA AGA GGA ACG TTC CCC CAG GAA AAC	1051
Gln Ile Gly Gln Leu Val Gly Ala Arg Gly Thr Phe Pro Gln Glu Asn	
185 190 195	
AAG GAG GAC TGC AAG CCT TGT GAG GGT CCC AAG AAG ACT GTT GAA ACT	1099
Lys Glu Asp Cys Lys Pro Cys Glu Gly Pro Lys Lys Thr Val Glu Thr	
200 205 210	
ACT TCT GAG AAA TGT AAT CTT GGG TGC GAG CTT AAA GGA ACA TCT GCT	1147
Thr Ser Glu Lys Cys Asn Leu Gly Cys Glu Leu Lys Gly Thr Ser Ala	
215 220 225 230	
CTG ATA AGC AAG GCC ATA CAG AAG AAG GAA GTC AAG GAC ACG AAG GAA	1195
Leu Ile Ser Lys Ala Ile Gln Lys Lys Glu Val Lys Asp Thr Lys Glu	
235 240 245	
GGG GAG AAA AGT GCA AGC CAG GAC TCT GAT GGC GAG GGC ACT GCT GAG	1243
Gly Glu Lys Ser Ala Ser Gln Asp Ser Asp Gly Glu Gly Thr Ala Glu	
250 255 260	
GAT GCG GAA GTA CAG CAA CCT TCT GCG GAC GGC GAG GGT CTA GAG TAA	1291
Asp Ala Glu Val Gln Gln Pro Ser Ala Asp Gly Glu Gly Leu Glu	
265 270 275 277	
TTTTTAAATT AAAATCTCCC TGGATTGAAT CTTCAAGTGC TTTTGTGAAA GACTTTGGGA	1351
ACATTTCTGTG AAGGCTAACA TAAATTGTTA ATCTCAGGTC ACTCGATGGA ATAGTCAATT	1411
CGTATTTTCCT TTCCTTGGAT GGTCTGCCCC ACCAGCCTGT TCCTGGCAGT TATCGCATCG	1471
TCGACAGAGT CAAACTGAAC GAATCCATAT CCTTTGGACA TCTTCTTGTA TTGGTCGTAG	1531
ACTATTACTA CCCGATAGTT CAGTATCTCA CTGATCCTCT CCTTGAGAAG GTCTCTAACG	1591

TCGTCCTTCGG TTATGTGTGC TCCCAGCCCCA AATATCCCTA TCGCCCTGGA GGGAGACCCG	1651
TTTCTCTTTG CTTTAAGTGC ATATCTTTTCG TTTTATAGG AGCTTGATC TGTTCTTCG	1711
TATCCCCTTG TCGGGCGCTC CACCTCGAG	1740

(2) INFORMATION FOR SEQ ID No: 3

(i) CHARACTERISTICS OF THE SEQUENCE:

(A) LENGTH:

(B) TYPE: nucleotide

(C) NUMBER OF STRANDS: double

(D) CONFIGURATION: linear

(ii) TYPE OF MOLECULE: DNA

(ix) CHARACTERISTICS

(A) NAME/KEY:

(xi) DESCRIPTION OF THE SEQUENCES: SEQ ID No: 3:

ATG AAA GGT ATT TCT AAG GTT CTC TCA GCC TCT ATT GTC CTA ATG AAG	48
Met Lys Gly Ile Ser Lys Val Leu Ser Ala Ser Ile Val Leu Met Lys	
1 5 10 15	
TTG AAG GGT GTC TAT TCT ACA ACT GTG CTG TGT GGA GAT TCA ACA CAA	96
Leu Lys Gly Val Tyr Ser Thr Thr Val Leu Cys Gly Asp Ser Thr Gln	
20 25 30	
GGA CTG CAG GGC ACA ACC CAA CCG TCA TAT GTG CTG GTT CCT AGT GCA	144
Gly Leu Gln Gly Thr Thr Gln Pro Ser Tyr Val Leu Val Pro Ser Ala	
35 40 45	
CCA GAG ACA ATA GCC AAC TGT GGA TAC AGT CCA CAG AAC ATG TAT GTC	192
Pro Glu Thr Ile Ala Asn Cys Gly Tyr Ser Pro Gln Asn Met Tyr Val	
50 55 60	
CCT TCT ACT CCT ACT ACC ATG CCT TCC ACA GTG CCA GGC ACA ACT GGT	240
Pro Ser Thr Pro Thr Thr Met Pro Ser Thr Val Pro Gly Thr Thr Gly	
65 70 75 80	
GAG AGC GAG ACA CCT ACT TCT CCA ACA TCA TCT CCT ACA GAG GAT GTG	288
Glu Ser Glu Thr Pro Thr Ser Pro Thr Ser Ser Pro Thr Glu Asp Val	
85 90 95	
GGA ACA TGC AAG ATT GCT GTT GTA AAG CAT TGT GAT GCA CCA GGA ACA	336
Gly Thr Cys Lys Ile Ala Val Val Lys His Cys Asp Ala Pro Gly Thr	
100 105 110	
TCA TCA ACA CCT TGC GAA CCG GAA CAG ACT TTG GCC CCC TCT CAG CCA	384
Ser Ser Thr Pro Cys Glu Pro Glu Gln Thr Leu Ala Pro Ser Gln Pro	
115 120 125	
GTA GCA GCT ACA ATT GCC ACA CCA CTG GTT GPT GCT TCT GTG CAG ACG	432
Val Ala Ala Thr Ile Ala Thr Pro Leu Val Val Ala Ser Val Gln Thr	
130 135 140	
CCG CAA GCA GCT GTT ACC ATC CTT ACT CCA AAG GCC GTC TCT GCC CAG	480
Pro Gln Ala Ala Val Thr Ile Leu Thr Pro Lys Ala Val Ser Ala Gln	
145 150 155 160	

CCG GCA ACC ATC ATT TCT CCA TTC AAC CAG GCA CCA GGC TAC TAC AAT	528
Pro Ala Thr Ile Ile Ser Pro Phe Asn Gln Ala Pro Gly Tyr Tyr Asn	
165 170 175	
AGT GCA ATT CCC GGG CAA ATA CTT ACA GGT AAT GTT CTC TCT CCA AGT	576
Ser Ala Ile Pro Gly Gln Ile Leu Thr Gly Asn Val Leu Ser Pro Ser	
180 185 190	
GCC TCT TCT TGC CAA GTG GTG CCC GGA ACA ACA GGA AGC TCC ACC CCC	624
Ala Ser Ser Cys Gln Val Val Pro Gly Thr Thr Gly Ser Ser Thr Pro	
195 200 205	
CAG CAG CTA CCA GGC GCT GTT TCA TCT GGA ACC ATT CCT TGC CAA ATA	672
Gln Gln Leu Pro Gly Ala Val Ser Ser Gly Thr Ile Pro Cys Gln Ile	
210 215 220	
GTA CAG GGA ACT CAA AGT AGC GGA AAC ACC CCT GGA CAG CAA TTC TTG	720
Val Gln Gly Thr Gln Ser Ser Gly Asn Thr Pro Gly Gln Gln Phe Leu	
225 230 235 240	
CCG GGA ATC GTT CCT GTT GGA AGC CTC CAG CCG GAT CAA GCT ACT TCT	768
Pro Gly Ile Val Pro Val Gly Ser Leu Gln Pro Asp Gln Ala Thr Ser	
245 250 255	
GGA ACC CCT ACC CCT TCT GTT AGC CAA AGC CAA TCT GGA CAG CAA TGC	816
Gly Thr Pro Thr Pro Ser Val Ser Gln Ser Gln Ser Gly Gln Gln Cys	
260 265 270	
TGC TGC ACT CCT CCA ATC ACA AAC CCT GTA ATG CCA ACT CCT ATG GGT	864
Cys Cys Thr Pro Pro Ile Thr Asn Pro Val Met Pro Thr Pro Met Gly	
275 280 285	
ATC AGC AGT AAT GGG TAT CCC AGC TCA ACT GCG TAC GCC CCA ACC CTT	912
Ile Ser Ser Asn Gly Tyr Pro Ser Ser Thr Ala Tyr Ala Pro Thr Leu	
290 295 300	
GGA CAA TTG GGA CCT TGC ATC GAC ACA CAG AAG TCA ACA TCA TCC TGC	960
Gly Gln Leu Gly Pro Cys Ile Asp Thr Gln Lys Ser Thr Ser Ser Cys	
305 310 315 320	
GAA CCA AAA GAA AAG CCT GTA GCA CAG TAT GGA ATG GAA GCA TGC GCT	1008
Glu Pro Lys Glu Lys Pro Val Ala Gln Tyr Gly Met Glu Ala Cys Ala	
325 330 335	
GCA CCA ACT CCA ACT GCT GTT CTA GGA AAT GCT GAG TAT CTC CTT AGC	1056
Ala Pro Thr Pro Thr Ala Val Leu Gly Asn Ala Glu Tyr Leu Leu Ser	
340 345 350	
CCG GGG ATG TAT AAT TCA CTC AAC TCT CCA TGC AAC GCT TGC TGC CAA	1104
Pro Gly Met Tyr Asn Ser Leu Asn Ser Pro Cys Asn Ala Cys Cys Gln	
355 360 365	
CAA CAA TGC TAG	1116
Gln Gln Cys *	
370 371	

(2) INFORMATION FOR SEQ ID No: 4

(i) CHARACTERISTICS OF THE SEQUENCE:

(A) LENGTH:

(B) TYPE: nucleotide

(C) NUMBER OF STRANDS: double

(D) CONFIGURATION: linear  
(ii) TYPE OF MOLECULE: DNA  
(ix) CHARACTERISTICS  
(A) NAME/KEY:  
(xi) DESCRIPTION OF THE SEQUENCES: SEQ ID No: 4:

ATG TTG TTA CTT CTC TCA GCA GTT GCT TTT GTT AGC GCT ACA GCA GTC	48
Met Leu Leu Leu Leu Ser Ala Val Ala Phe Val Ser Ala Thr Ala Val	
1 5 10 15	
CAG TCA GGT GTT GTC TCC CAG CCT ACA ACA CCC ATT CCG ATT CTT CCT	96
Gln Ser Gly Val Val Ser Gln Pro Thr Thr Pro Ile Pro Ile Leu Pro	
20 25 30	
GGA CAG CCG ATG GGG GGC ATG GCC AAC GGG TGC ACT AAC AAG AAA CTA	144
Gly Gln Pro Met Gly Gly Met Ala Asn Gly Cys Thr Asn Lys Lys Leu	
35 40 45	
GAT GGT GTT GAA ATA ATG AGA AGG AAC ATG GTG GAA TGC CAG AAG AGA	192
Asp Gly Val Glu Ile Met Arg Arg Asn Met Val Glu Cys Gln Lys Arg	
50 55 60	
AAT GCA GAG GCA ACA AAA GCA ATG GTT GAA AGG GCT AAT GAA AAG GCT	240
Asn Ala Glu Ala Thr Lys Ala Met Val Glu Arg Ala Asn Glu Lys Ala	
65 70 75 80	
GTA GAA ACA TTC AAT AAG GAG GTC AGT AAA GGA CCT CAA AAG GAA AGC	288
Val Glu Thr Phe Asn Lys Glu Val Ser Lys Gly Pro Gln Lys Glu Ser	
85 90 95	
GGC CAG TGC ATA GAA AAA GCT GTA CAG GGC ACC GAC AGA TGT ATT CTT	336
Gly Gln Cys Ile Glu Lys Ala Val Gln Gly Thr Asp Arg Cys Ile Leu	
100 105 110	
GCA GGA ATA ATT GAT AAG GCT GTG AAC AAG CGT AAG TAC AGA ATC TCG	384
Ala Gly Ile Ile Asp Lys Ala Val Asn Lys Arg Lys Tyr Arg Ile Ser	
115 120 125	
GAT GTG GAG AAT AGC ACC TCG CTC TAT AGA GGC GAC AAA CTA ATT GCT	432
Asp Val Glu Asn Ser Thr Ser Leu Tyr Arg Gly Asp Lys Leu Ile Ala	
130 135 140	
CTA ATT GTC AAT GTT GAC TAT GGA CTT CAG CCA ATT ATC AAA CCA AAG	480
Leu Ile Val Asn Val Asp Tyr Gly Leu Gln Pro Ile Ile Lys Pro Lys	
145 150 155 160	
AAG AAG AAA TCC AAG ATA ATG GCA AAT CTT CCT CAA CCA AAG AGA GAG	528
Lys Lys Lys Ser Lys Ile Met Ala Asn Leu Pro Gln Pro Lys Arg Glu	
165 170 175	
ATG TAT TTC AAC CAG ATC GGA CAG CTT GTT GGA GCA AAG GGA ACA TTC	576
Met Tyr Phe Asn Gln Ile Gly Gln Leu Val Gly Ala Lys Gly Thr Phe	
180 185 190	
CCT CAA GAC AAC AAG GAT GAA TGC AAG CCA TGC GAA CCT AAG AAG ACT	624
Pro Gln Asp Asn Lys Asp Glu Cys Lys Pro Cys Glu Pro Lys Lys Thr	
195 200 205	
GTT GAA ACT GCT TCT GAA AGA TGT AAT CTT GGG TGC GAG CTT AAG GGA	672
Val Glu Thr Ala Ser Glu Arg Cys Asn Leu Gly Cys Glu Leu Lys Gly	
210 215 220	





